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1 GTCGACCCACCGTCCGGCAGCAGGCAGGCTGCAGCAGGCAGCAGCAGCAAGAGTAAAAGG  
CAGCTGGGTGCGCAGGCCGTCCGTCCGACGTGTCCTCGCTCGTCTCAATTTC  
-----

63 TGACCGCGGCTGCCACCCCAGAGCCATGGGGCGGGCACGAGATGCCATCCTGGACGCTCTT  
ACTGGCGCCGACGGGTGGGGTCTCGTACCCGCCGTGCTCTACGGTAGGACCTGCGAGAA  
1► M G R A R D A I L D A L -----

125 GAAAAACTTGTCAAGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCG  
CTTTGAACAGTCCCCTACTTGTAGTTCAAGTTCTACTTCGACGACTGTCACGTTGACGC  
13► E N L S G D E L K K F K M K L L T V Q L R -----

187 AGAAGGCTATGGGCGCATCCACGGGGGGCCCTGCTGCAGATGGACGCCATAGATCTCACTG  
TCTTCCGATAACCGCGTAGGGTGCACGGGACGACGTCTACCTGCGGTATCTAGAGTGAC  
33► E G Y G R I P R G A L L Q M D A I D L T -----

249 ACAAACTTGTCAAGCTACTATCTGGAGTCGTATGGCTTGGAGCTACAATGACTGTGCTTAGA  
TGTGAAACAGTCGATGATAGACCTCAGCATAACCGAACCTCGAGTGTACTGACACGAATCT  
54► D K L V S Y Y L E S Y G L E L T M T V L R -----

311 GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGAAGAGTCTGGAGCTGT  
CTGTACCCGAATGTCTCGACCGACTCGTCGACGTTGCTGATTCTCTCAGACCTCGACA  
75► D M G L Q E L A E Q L Q T T K E E S G A V -----

373 GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTGTGGACCAGC  
CCGTCGACGTCGGTACAGGGACGAGTCTCATGTCGGTCTGTGCTGTAAACACCTGGTCG  
95► A A A A S V P A Q S T A R T G H F V D Q -----

435 ACAGGCAAGCACTCTTGCACAGGGTCACAGAAGTGGACGGAGTGTGGATGCTTGCATGGC  
TGTCCGTTGAGTAACGGTCCCAGTGTCTTACCTGCTCACGACCTACGAAACGTACCG  
116► H R Q A L I A R V T E V D G V L D A L H G -----

497 AGTGTGCTGACTGAAGGACAGTACCAAGGAGTTCTGTCAGAGACCAAGGACCAAGACAAGAT  
TCACACGACTGACTTCTGTCAAGGACGTTCTGTCAGAGACCAAGGACCAAGACAAGAT  
137► S V L T E G Q Y Q A V R A E T T S Q D K M -----

559 GAGGAAGCTCTCAGCTTGTCCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG  
CTCCCTCGAGAAGTCGAAACAAGGTAGGACCTGGACTGGACGTTCTGAGGGAGGAGGTCC  
157► R K L F S F V P S W N L T C K D S L L Q -----

621 CCTTGAAGGAAATACATCCCTACTTGGTATGGACCTGGAGCAGAGCTGAGGTATCTTTCC  
GGAACCTCCCTTATGTAGGGATGAACCAACTACCTGGACCTCGTCGACTCCATAGAAAAGG (SEQ ID NO:3)  
178► A L K E I H P Y L V M D L E Q S (SEQ ID NO:2) -----

683 AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTGGAAAAAAACAATTGTATTGT  
TCGATGTAATAGATCGAGGACTGAAACATATGTGTTAAAACCTTTGTAAACATAAAC  
-----

745 GTTTAAAAAAAAAAAAAAAGGGCGGCCGC (SEQ ID NO:1)  
CAAATTTTTTTTTTTTCCCGCCGGCG -----

FIG. 1

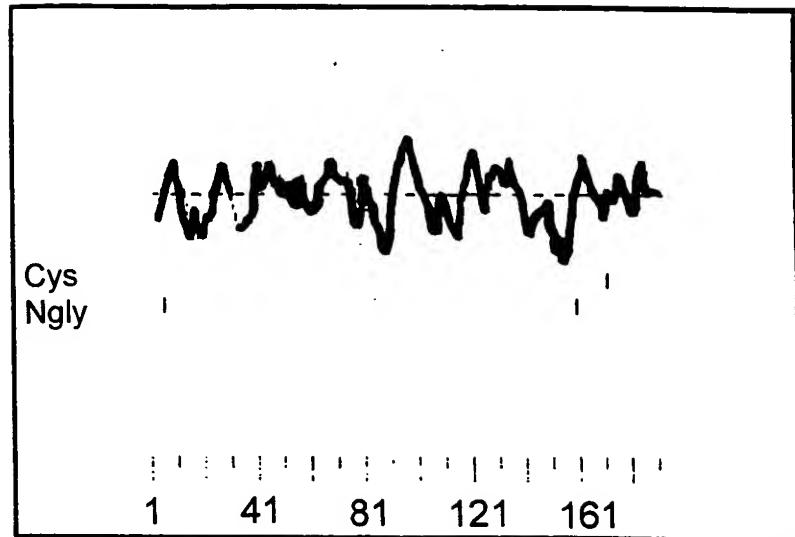


FIG. 2

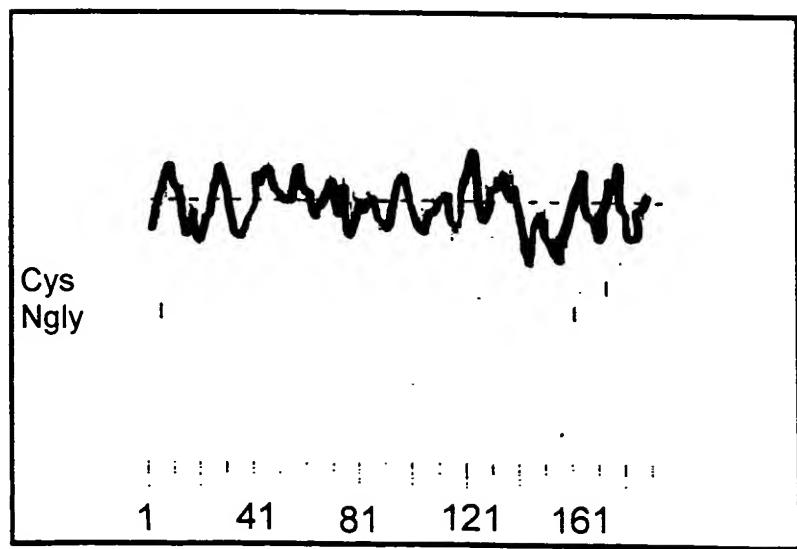


FIG. 4

1 CGCGTCCGGCTGCAGCAGGGTGAGCGGCGGCAGCGGCCGGGGATCCTGGAGCCATGGGC  
GCGCAGGCCGACGTGCCCCACTCGCCGCCGTGCCGCCCCTAGGACCTCGGTACCCCG

1► M G

61 CGCGCGCGACGCCATCCTGGATCGCTGGAGAACCTGACCGCCAGGAGCTAAGAAGT  
CGCGCGCTGCGGTAGGACCTACGCGACCTCTGGACTGGCGCTCTCGAGTTCTCA  
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTCGGTGCCGCTGCGCGAGGGCTACGGGCGCATCCCGCGGGCG  
AGTTCGACTTCGACGACAGCCACGGCGACGGCGCTCCCGATGCCCGTAGGGCGCCCCCGC  
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGACGCCCTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA  
GCGACGACAGGTACCTGGCGAACCTGGAGTGGCTGTCGACCAGTCGAAGATGGACCTCT  
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCCGAGCTCACCGCTAACGTGCTGCGCAGATGGGCTGCGAGGAGATGGCG  
GGATGCCCGGGCTCGAGTGGCGATTGACCGACGCGCTGTACCCGGACGTCCTCTACCGGC  
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGGCACGCACCGAACCCAGGGCTCTGGAGCCGCCAGCTGGATCCAGGCC  
CCGTCGACGTCCGCCGTGCGTGGTCCCAGACCTCGGCCGGTCGACCCCTAGGTCCGGG  
83► G Q L Q A A T H Q G S G A A P A G I Q A

361 CTCCTCAGTCGGCAGCCAAGCCAGGCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA  
GAGGAGTCAGCCGTGGTCCGGACGTGAAATATCTGGTCGTGGCCCCACGGCAAT  
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTAAGGGAAAGTCCTGACGG  
AGCGCTCCAGTGTGCAACTCACCGACGACCTACCGAGACATGCCCTCCAGGACTGCC  
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAAGGCAAGTGGCTGCTGGATGCTCTGTAAGGGAAAGTCCTGACGG  
TACTCGTCATGGTCCGTACGCCGGCTGGTGGTTGGTTCTACGCCCTCGAGA  
143► D E Q Y Q A V R A E P T N P S K M R K L

541 TCAGTTCACACCAGCCTGGAACCTGGACCTGCAAGGACTTGCTCCAGGCCCTAACGG  
AGTCAGGACTGTGGTCCGACCTTGACCTGGACGTTCTGAAAGGAGGTCCGGATTCCC  
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCAGTCCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCTTCCAGCAACAC  
TCAGGGTCAGGATGGACCACTCCTGGACCTCGCTCGACTCCGAGGAAGGGCGTTGTG (SEQ ID NO:6)  
183► E S Q S Y L V E D L E R S (SEQ ID NO:5)

661 TCCGGTCAGCCCCCTGGCAATCCACCAAATCATCCTGAATCTGATCTTTTATACACAAT  
AGGCCAGTCGGGGACCGTTAGGGTGGTTAGTAGGACTTAGACTAGAAAAATATGTGTTA

721 ATACGAAAAGCCAGCTTGAA (SEQ ID NO:4)  
TATGCTTTCGGTGCAACTT

FIG. 3

FIG. 5A

FIG. 5B

ALIGN calculates a global alignment of two sequences

version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

> hCARD5-protein 195 aa vs.

> mCARD5-protein 193 aa

scoring matrix: pam120.mat, gap penalties: -12/-4

71.8% identity; Global alignment score: 712

10	20	30	40	50	60
inputs MGRARDAILDALENLTAEEKKFKLKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSFY					
::: :::::::::::::::					
MGRARDAILDALENLSGDELKKFKMKLTVQLREGYGRIPRGALLQMDAIDLTDKLVSYY					
10	20	30	40	50	60
70	80	90	100	110	120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA					
::::: :::: ::::::::::: ::::: : . ::::::. . ::::::. : :::::::					
LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ					
70	80	90	100	110	
130	140	150	160	170	180
inputs ALIARVTNVEWLLDALYGVLTDEQYQAVRAEPTNPSKMRKLFSTPAWNWTCKDLLLQA					
::::::::: . ::::: : ::::: ::::::::::: ::::::::::: ::::: :::::					
ALIARVTEVDGVLDALHGSVLTEGQQYQAVRAETTSQDKMRKLFSTVPSWNLTCKDSSLQA					
120	130	140	150	160	170
190					
inputs LREQSYLVEDLERS (SEQ ID NO:5)					
::: . :::: : ::::					
LKEIHPYLVMDLEQS (SEQ ID NO:2)					
180	190				

FIG. 6

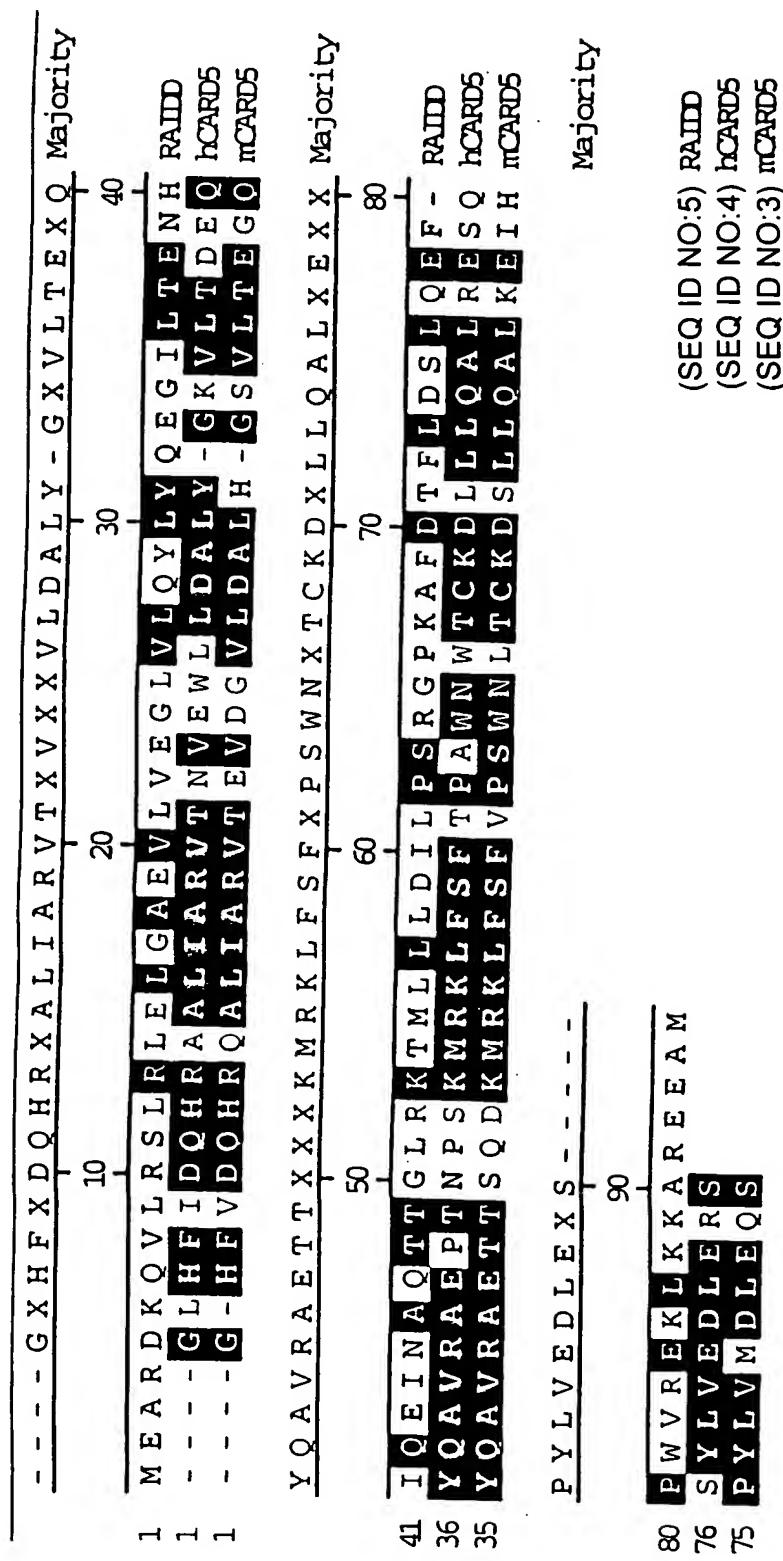


FIG. 7

- A - E S - G S E I I D 0 H R X A L L A R V T E D P - D S L L D A L L S R D L I Majority

1	I A Q Q W - - - - -	I Q S K P R E D I V N Q M T E A C L N Q S L D A L L S R D L I	40
1	- - E S H P H I Q L K S N R E L L V T H I R N T - Q C L V D N L K N F Y F	30	
1	- - - - C L H F I D Q H R A A L I A R V T N - - V E W V L D A L Y G K - V L	20	
1	- - - - C - H F V D O H R Q A L I A R V T E - - V D G V L D A L H G S - V L	10	
1	- - - - M A T E S T P S E I I E R E R K K L L E I L Q H D F - D S I L D T L T S R R L I		
1	- - - - M A S E G A S S E I I E K Q R T K I L L S V I L Q Q D P - D S I L D T I T S R R L I		

36	M K E D Y E L V S T K P T R T S K V R Q L L D T T D I Q G E E - - - F A F V I	H CARD3-CARD
37	S A E D A F I V C A C P T Q P D K V R K I I D L V O S K G E E V S E F F I - Y L	H CARD4-CARD
32	T D E Q Y Q A V R A E P T N P S K M R K L F S F T P A W - N W T C K - - - D L L	H CARD5-CARD
31	T E G Q Q Y Q A V R A E T T S Q D E M R K L F S F V P S W - N L T C K - - - D S L	H CARD6-CARD
40	S E E E Y E T L E N V T D L E K S R K L L V Q K G E A T C Q H F L K C L C C F L K C L	H CARD6-CARD
40	S E E E Y E T L E A I T D P L K K S R K L L V Q K G E A T C Q H F L K C L C C F L K C L	H CARD6-CARD

LOA LKDSA AXYL GLDPEV - - - - - LE - S (SEQ ID NO:12) Majority

8  
G  
E